

# Preparation for Term Paper (Genomic Heritability Calculations)

# Review from [Barry et al. 2023](#) (*Figure 1*)

- **Family Based Designs**
  - Twin studies
  - Extended Twin Design (including other relatives)
- **Genomic Methods: Unrelated Individuals**
  - Linkage Disequilibrium (*LD*) Score Regression
    - Supplemental Materials describe implementation in [LDSC](#) package ([Bulik-Sullivan et al. 2015](#)).
  - Genomic relatedness REstricted Maximum-Likelihood (***GREML***)
    - Part of [GCTA](#) (Genome-wide Complex Trait Analysis, [Yang et al. 2011](#))
    - [GCTA Wikipedia Entry](#)
  - LD- and MAF-stratified GREML (*GREML-LDMS*, [Yang et al. 2015](#))
- **Genomic Methods: Related Individuals**
  - *GREML-KIN* (GREML with KINship analysis – [Hill et al. 2018](#), [Xia et al. 2016](#), and/or [Zaitlen et al. 2013](#).
    - On the *GCTA* website, the section for “*GREML in family data*” references [Zaitlen et al. 2013](#).
  - *Trio-GCTA* ([Eilertsen et al. 2021](#))
  - Material (or Paternal) GCTA (*M-GCTA*, [Qiao et al. 2020](#))
  - Relatedness Disequilibrium Regression (***RDR***, [Young et al. 2018](#))
    - Supplemental Materials also reference [Visscher et al. 2006](#).
- *Table 1* also describes strengths and limitations, which include the relative estimated contribution of rare variants.
- *Box 1* defines narrow-sense heritability versus broad sense heritability.

# Methods for *Unrelated* Individuals

- Genomic relatedness REstricted Maximum-Likelihood (***GREML***)

# Methods Considering *Related* Individuals

- Relatedness Disequilibrium Regression (**RDR**, [Young et al. 2018](#))

# Additional Reviews

(referenced by [Barry et al. 2023](#))

- In addition to the [Visscher et al. 2010](#) height GWAS article mentioned in the [Height QTL Notes](#), [Barry et al. 2023](#) reference a review related to heritability and genomics in [Visscher et al. 2008](#).
- A review by [Mayhew et al. 2017](#) is also referenced.
- [Yang et al. 2017](#) includes a figure related to estimation of height heritability with *different methods*.
- [Young 2019](#) includes a table showing variation in heritability values for height (with *different methods* and in different cohorts).
- [Zhu and Zhou 2020](#) is another cited review.

# Previous Related Discussions

- I have a *journal comment/question* for [Young 2019](#), which was referenced in the [Barry et al. 2023](#) review.
- I have a *preprint comment* for [Dolan et al. 2019](#), which specifically references **RDR** (in reference to *Young 2019* comment/question above) as well as **heritability**.
- I have *preprint comment* on an article titled “[Recovery of trait heritability from whole genome sequence data](#)” (with a later peer-reviewed version published in [Wainschtein et al. 2022](#)).
- As might be expected, “*heritability*” is mentioned in the [earlier preprint comment](#) for the *Bloom et al. 2019* data that I am (partially) [re-analyzing](#).
- Because data analysis was not performed, it may be somewhat off topic. However, there was mention to interpretation of heritability in a *preprint comment* on [Lowes et al. 2022](#).
- While not exactly about heritability, I have a *preprint comment* related to predicting height for [Thompson et al. 2022](#).
- Height is also briefly mentioned in a *Disqus* comment for [Marnetto et al. 2020](#), even if not currently visible on the journal website?.

# Newer/Additional Methods

- *GPLEMMA* ([Kerin and Marchini 2020](#))
  - Cites *RDR* publication ([Young et al. 2018](#))
- *SAFE-h<sup>2</sup>* ([Darbani and Nicolaisen 2023](#))
  - Includes comparisons to *EMMAX* ([Kang et al. 2010](#)) and *LDAK*.
  - *EMMAX* = EMMA eXpedited, an extension of EMMA ([Kang et al. 2008](#)).
  - Two implementations for *LDAK* are mentioned. One is within *GCTA*, and the other is described as *LDAK-Thin* ([Speed et al. 2012](#)).
- The [GCTA webpage](#) lists *sBLUP* among available methods, but not necessarily for heritability?
  - *sBLUP* = Summary-level BLUP
  - Best Linear Unbiased Prediction ([BLUP](#)) is referenced in [Wang et al. 2019](#)
  - The *rrBLUP* (ridge-regression BLUP) R-package is a [dependency](#) for the *Bloom et al. 2019* code (imported in [mapping.R](#), for example).
- While not an additional method, [Tang et al. 2022](#) is an additional review on the general topic.
  - Includes descriptions of additional methods.
- [Srivastava et al. 2023](#) is another such review.
  - Describes [REML](#) (REstricted Maximum Likelihood, with applications in [Lee et al. 2006](#) and [Yang et al. 2010](#)) for individual-level data, before listing assumptions for *GREML* versus *LDAK*.
- [Evans et al. 2018](#) provides a comparison of different methods.
  - It looks like there is noticeable emphasis on implementation of *GREML* and *LDAK* methods.